

SEQUENCE LISTING

<110> Brenda F. Baker
Susan M. Freier

<120> ANTISENSE MODULATION OF INTERLEUKIN 8 EXPRESSION

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Met Thr Ser Lys Leu Ala Val Ala
1 5ctc ttg gca gcc ttc ctg att tct gca gct ctg tgt gaa ggt gca gtt 162
Leu Leu Ala Ala Phe Leu Ile Ser Ala Ala Leu Cys Glu Gly Ala Val
10 15 20ttg cca agg agt gct aaa gaa ctt aga tgt cag tgc ata aag aca tac 210
Leu Pro Arg Ser Ala Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr
25 30 35 40tcc aaa cct ttc cac ccc aaa ttt atc aaa gaa ctg aga gtg att gag 258
Ser Lys Pro Phe His Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu
45 50 55agt gga cca cac tgc gcc aac aca gaa att att gta aag ctt tct gat 306
Ser Gly Pro His Cys Ala Asn Thr Glu Ile Ile Val Lys Leu Ser Asp
60 65 70gga aga gag ctc tgt ctg gac ccc aag gaa aac tgg gtg cag agg gtt 354
Gly Arg Glu Leu Cys Leu Asp Pro Lys Glu Asn Trp Val Gln Arg Val
75 80 85gtg gag aag ttt ttg aag agg gct gag aat tca taa aaaaattcat 400
Val Glu Lys Phe Leu Lys Arg Ala Glu Asn Ser
90 95 100

tctctgttgtt atccaagaat cagtgaagat gccagtgaaa cttcaagcaa atctactca 460

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RTS-0266

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Ala Ala Phe Leu Ile Ser Ala Ala Leu Cys Glu Gly Lys His Ile Phe

15

RTS-0266

ctg acc tac agc gtt ttc cta tgt cta aat gtg atc ctt aga tag caa Leu Thr Tyr Ser Val Phe Leu Cys Leu Asn Val Ile Leu Arg * Gln 30 35 40	1709
agc tat tct tga tgc ttt ggt aac aaa cat cct ttt tat tca gaa aca Ser Tyr Ser * Cys Phe Gly Asn Lys His Pro Phe Tyr Ser Glu Thr 45 50 55	1757
gaa tat aat ctt agc agt caa tta atg tta aat tga aga ttt aga aaa Glu Tyr Asn Leu Ser Ser Gln Leu Met Leu Asn * Arg Phe Arg Lys 60 65 70	1805
aac tat ata taa cac tta gga aat ata aag gtt tga tca ata tag ata Asn Tyr Ile * His Leu Gly Asn Ile Lys Val * Ser Ile * Ile 75 80	1853
ttc tgc ttt tat aat tta tac cag gta gca tgc ata tat tta acg taa Phe Cys Phe Tyr Asn Leu Tyr Gln Val Ala Cys Ile Tyr Leu Thr * 85 90 95	1901
ata agt aat tta tag tat gtc cta ttg aga acc acg gtt acc tat att Ile Ser Asn Leu * Tyr Val Leu Leu Arg Thr Thr Val Thr Tyr Ile 100 105 110	1949
atg tat taa tat tga gtt gag caa ggt aac tca gac aat tcc act cct Met Tyr * Tyr * Val Glu Gln Gly Asn Ser Asp Asn Ser Thr Pro 115 120 125	1997
tgt agt att tca ttg aca agc ctc aga ttt gtc att aat tcc tgt ctg Cys Ser Ile Ser Leu Thr Ser Leu Arg Phe Val Ile Asn Ser Cys Leu 130 135 140	2045
gtt taa aga tac cct gat tat aga cca ggc atg tat aac tta ttt ata Val * Arg Tyr Pro Asp Tyr Arg Pro Gly Met Tyr Asn Leu Phe Ile 145 150 155	2093
tat ttc tgt taa ttc ttt ctg aag gca att tct atg ctg gag agt ctt Tyr Phe Cys * Phe Phe Leu Lys Ala Ile Ser Met Leu Glu Ser Leu 160 165 170	2141
agc ttg cct act ata aat aac act gtg gta tca cag agg att atg caa Ser Leu Pro Thr Ile Asn Asn Thr Val Val Ser Gln Arg Ile Met Gln 175 180 185 190	2189

DRAFTED - EDITED - PROOFED

tat tga cca gat aaa aat acc atg aag ttg ata ttg tac aaa aag Tyr * Pro Asp Lys Asn Thr Met Lys Met Leu Ile Leu Tyr Lys Lys 195 200 205	2237
aac tct aac tct tat ata gga agt tgt tca atg ttg tca gtt atg act Asn Ser Asn Ser Tyr Ile Gly Ser Cys Ser Met Leu Ser Val Met Thr 210 215 220	2285
gtt ttt taa aac aaa gaa cta act gag gtc aag ggc tag gag ata ttc Val Phe * Asn Lys Glu Leu Thr Glu Val Lys Gly * Glu Ile Phe 225 230 235	2333
agg aat gag ttc act aga aac atg atg cct tcc ata gtc tcc aaa taa Arg Asn Glu Phe Thr Arg Asn Met Met Pro Ser Ile Val Ser Lys *240 245 250	2381
tca tat tgg aat tag aag gaa gta gct ggc aga gct gtg cct gtt gat Ser Tyr Trp Asn * Lys Glu Val Ala Gly Arg Ala Val Pro Val Asp 255 260 265	2429
aaa atc aat cct taa tca ctt ttt ccc cca aca ggt gca gtt ttg cca Lys Ile Asn Pro * Ser Leu Phe Pro Pro Thr Gly Ala Val Leu Pro 270 275 280	2477
agg agt gct aaa gaa ctt aga tgt tgc ata aag aca tac tcc aaa Arg Ser Ala Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys 285 290 295	2525
cct ttc cac ccc aaa ttt atc aaa gaa ctg aga gtg att gag agt gga Pro Phe His Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu Ser Gly 300 305 310	2573
cca cac tgc gcc aac aca gaa att atg taa gta ctt taa aaa aga tta Pro His Cys Ala Asn Thr Glu Ile Met * Val Leu * Lys Arg Leu 315 320 325	2621
gat att ttg ttt tag caa act taa aat taa gga agg tgg aaa tat tta Asp Ile Leu Phe * Gln Thr * Asn * Gly Arg Trp Lys Tyr Leu 330 335	2669
gga aag ttc cag gtg tta gga tta cag tag taa atg aaa caa aac aaa Gly Lys Phe Gln Val Leu Gly Leu Gln * * Met Lys Gln Asn Lys 340 345 350	2717

RTS-0266

ata aaa ata ttt gtc tac atg aca ttt aaa tat ggt agc ttc cac aac Ile Lys Ile Phe Val Tyr Met Thr Phe Lys Tyr Gly Ser Phe His Asn 355	360	365	2765	
tac tat aaa tgt tat ttt gga ctt aga ctt tat gcc tga ctt aag gaa Tyr Tyr Lys Cys Tyr Phe Gly Leu Arg Leu Tyr Ala * Leu Lys Glu 370	375	380	2813	
tca tga ttt gaa tgc aaa aac taa ata tta atc tga acc att tct ttc Ser * Phe Glu Cys Lys Asn * Ile Leu Ile * Thr Ile Ser Phe 385	390	395	2861	
tta ttt cag tgt aaa gct ttc tga tgg aag aga gct ctg tct gga ccc Leu Phe Gln Cys Lys Ala Phe * Trp Lys Arg Ala Leu Ser Gly Pro 400	405	410	2909	
caa gga aaa ctg ggt gca gag ggt tgt gga gaa gtt ttt gaa gag gta Gln Gly Lys Leu Gly Ala Glu Gly Cys Gly Glu Val Phe Glu Glu Val 415	420	425	2957	
agt tat ata ttt ttt aat tta aat ttt tca ttt atc ctg aga cat ata Ser Tyr Ile Phe Phe Asn Leu Asn Phe Ser Phe Ile Leu Arg His Ile 430	435	440	3005	
atc caa agt cag cct ata aat ttc ttt ctg ttg cta aaa atc gtc att Ile Gln Ser Gln Pro Ile Asn Phe Phe Leu Leu Lys Ile Val Ile 445	450	455	460	3053
agg tat ctg cct ttt tgg tta aaa aaa aag gaa tag cat caa tag tga Arg Tyr Leu Pro Phe Trp Leu Lys Lys Lys Glu * His Gln * * 465	470			3101
gtt tgt tgt act tat gac cag aaa gac cat aca tag ttt gcc cag gaa Val Cys Cys Thr Tyr Asp Gln Lys Asp His Thr * Phe Ala Gln Glu 475	480	485		3149
att ctg ggt tta agc ttg tgt cct ata ctc tta gta aag ttc ttt gtc Ile Leu Gly Leu Ser Leu Cys Pro Ile Leu Leu Val Lys Phe Phe Val 490	495	500		3197
act ccc agt agt gtc cta ttt tag atg ata att tct ttg atc tcc cta Thr Pro Ser Ser Val Leu Phe * Met Ile Ile Ser Leu Ile Ser Leu 505	510	515		3245

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RTS-0266-AUTHORSHIP

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COURT CLERK'S OFFICE

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RTS-0266 "CITROGENO"

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RTS-0266 - CH195601

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